



1600

RAW SEQUENCE LISTING

DATE: 06/12/2003

PATENT APPLICATION: US/09/917,265A

TIME: 14:29:42

Input Set : A:\IM-5.txt

Output Set: N:\CRF4\06122003\I917265A.raw

3 <110> APPLICANT: Wonderling, Ramani S.
 4 Boroughs, Karen L.
 6 <120> TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
 7 THEREOF
 9 <130> FILE REFERENCE: IM-5
 11 <140> CURRENT APPLICATION NUMBER: 09/917,265A
 12 <141> CURRENT FILING DATE: 2001-07-27
 14 <150> PRIOR APPLICATION NUMBER: 60/223,016
 15 <151> PRIOR FILING DATE: 2000-08-04
 17 <160> NUMBER OF SEQ ID NOS: 111
 19 <170> SOFTWARE: PatentIn version 3.2
 21 <210> SEQ ID NO: 1
 22 <211> LENGTH: 514
 23 <212> TYPE: DNA
 24 <213> ORGANISM: Felis catus
 27 <220> FEATURE:
 28 <221> NAME/KEY: CDS
 29 <222> LOCATION: (114)..(512)
 31 <220> FEATURE:
 32 <221> NAME/KEY: misc_feature
 33 <222> LOCATION: (470)..(470)
 34 <223> OTHER INFORMATION: n = unknown at position 470
 35 Xaa = unknown at position 119
 37 <400> SEQUENCE: 1
 38 gctaaagcg ctcctgccac cttctgccat ctacacagct caggaaaaga aaggacctc 60
 40 aaaccttcca gatcccttcc tctcttagga aactattgag cacagggata aag atg 116
 Met
 42 1
 44 act gct ata cca gta gat gat tgc atc aac ttt gtg gga atg aaa ttt 164
 45 Thr Ala Ile Pro Val Asp Asp Cys Ile Asn Phe Val Gly Met Lys Phe
 46 5 10 15
 48 att gac aat aca ctt tac ttt gta gct gac agt gat gaa aac ctg gaa 212
 49 Ile Asp Asn Thr Leu Tyr Phe Val Ala Asp Ser Asp Glu Asn Leu Glu
 50 20 25 30
 52 aca gat tac ttt ggc aag ctt gaa cat aaa ctc tca atc tta cga aac 260
 53 Thr Asp Tyr Phe Gly Lys Leu Glu His Lys Leu Ser Ile Leu Arg Asn
 54 35 40 45
 56 ttg aac gac caa gtt ctc ttc att aac cag gga gat caa cct gtg ttt 308
 57 Leu Asn Asp Gln Val Leu Phe Ile Asn Gln Gly Asp Gln Pro Val Phe
 58 50 55 60 65
 60 gag gat atg cct gat tct gac tgt aca gat aat gca ccc cgg act gaa 356
 61 Glu Asp Met Pro Asp Ser Asp Cys Thr Asp Asn Ala Pro Arg Thr Glu
 62 70 75 80

ENTERED

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64 ttt atc ata tat atg tat aaa gat agc ctc act aga ggt ctg gca gta      404
65 Phe Ile Ile Tyr Met Tyr Lys Asp Ser Leu Thr Arg Gly Leu Ala Val
66                85                90                95
68 acc atc tct gtg aat tat aag acc atg tct act ctc tcc tgt gag aac      452
69 Thr Ile Ser Val Asn Tyr Lys Thr Met Ser Thr Leu Ser Cys Glu Asn
70                100                105                110
W--> 72 aaa att att tcc ttt aan gga atg agt cct cct gag agt atc aat gat      500
73 Lys Ile Ile Ser Phe Xaa Gly Met Ser Pro Pro Glu Ser Ile Asn Asp
74                115                120                125
76 xaa gga aat gac at      514
77 Glu Gly Asn Asp
78 130
81 <210> SEQ ID NO: 2
82 <211> LENGTH: 133
83 <212> TYPE: PRT
84 <213> ORGANISM: Felis catus
86 <220> FEATURE:
87 <221> NAME/KEY: misc_feature
88 <222> LOCATION: (119)..(119)
89 <223> OTHER INFORMATION: The 'Xaa' at location 119 stands for Lys, or Asn.
91 <400> SEQUENCE: 2
93 Met Thr Ala Ile Pro Val Asp Asp Cys Ile Asn Phe Val Gly Met Lys
94 1                5                10                15
97 Phe Ile Asp Asn Thr Leu Tyr Phe Val Ala Asp Ser Asp Glu Asn Leu
98                20                25                30
101 Glu Thr Asp Tyr Phe Gly Lys Leu Glu His Lys Leu Ser Ile Leu Arg
102                35                40                45
105 Asn Leu Asn Asp Gln Val Leu Phe Ile Asn Gln Gly Asp Gln Pro Val
106                50                55                60
109 Phe Glu Asp Met Pro Asp Ser Asp Cys Thr Asp Asn Ala Pro Arg Thr
110 65                70                75                80
113 Glu Phe Ile Ile Tyr Met Tyr Lys Asp Ser Leu Thr Arg Gly Leu Ala
114                85                90                95
117 Val Thr Ile Ser Val Asn Tyr Lys Thr Met Ser Thr Leu Ser Cys Glu
118                100                105                110
W--> 121 Asn Lys Ile Ile Ser Phe Xaa Gly Met Ser Pro Pro Glu Ser Ile Asn
122                115                120                125
125 Asp Glu Gly Asn Asp
126                130
129 <210> SEQ ID NO: 3
130 <211> LENGTH: 514
131 <212> TYPE: DNA
132 <213> ORGANISM: Felis catus
135 <220> FEATURE:
136 <221> NAME/KEY: misc_feature
137 <222> LOCATION: (45)..(45)
138 <223> OTHER INFORMATION: n = unknown at position 45
140 <400> SEQUENCE: 3
W--> 141 atgtcatttc cttcatcatt gatactctca ggaggactca ttccnttaaa ggaaataatt      60

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143 ttgttctcac aggagagagt agacatggtc ttataattca cagagatggg tactgccaga 120
145 cctctagtga ggctatcttt atacatatat atgataaatt cagtccgggg tgcattatct 180
147 gtacagtcag aatcaggcat atcctcaaac acagggtgat ctccctgggt aatgaagaga 240
149 acttggtcgt tcaagtttcg taagattgag agtttatgtt caagcttgcc aaagtaatct 300
151 gtttccaggt tttcatcact gtcagctaca aagtaaagtg tattgtcaat aaatttcatt 360
153 cccacaaagt tgatgcaatc atctactggt atagcagtca tctttatccc tgtgctcaat 420
155 agtttcctaa gagaggaagg gatctggaag gtttgaggtc cttttctttt cctgagctgt 480
157 gtagatggca gaagggtggc ggagcgcctt tagc 514
160 <210> SEQ ID NO: 4
161 <211> LENGTH: 502
162 <212> TYPE: DNA
163 <213> ORGANISM: Felis catus
166 <220> FEATURE:
167 <221> NAME/KEY: CDS
168 <222> LOCATION: (3)..(464)
170 <220> FEATURE:
171 <221> NAME/KEY: misc_feature
172 <222> LOCATION: (126)..(126)
173 <223> OTHER INFORMATION: n = unknown at position 126
174 Xaa = unknown at position 42
176 <400> SEQUENCE: 4
177 gc aag ctt gaa cat aaa ctc tca atc tta cga aac ttg aac gac caa 47
178 Lys Leu Glu His Lys Leu Ser Ile Leu Arg Asn Leu Asn Asp Gln
179 1 5 10 15
181 gtt ctc ttc att aac cag gga gat caa cct gtg ttt gag gat atg cct 95
182 Val Leu Phe Ile Asn Gln Gly Asp Gln Pro Val Phe Glu Asp Met Pro
183 20 25 30
W--> 185 gat tct gac tgt aca gat aat gca ccc cgg nct gaa ttt atc ata tat 143
186 Asp Ser Asp Cys Thr Asp Asn Ala Pro Arg Xaa Glu Phe Ile Ile Tyr
187 35 40 45
189 atg tat aaa gat agc ctc act aga ggt ctg gca gta acc atc tct gtg 191
190 Met Tyr Lys Asp Ser Leu Thr Arg Gly Leu Ala Val Thr Ile Ser Val
191 50 55 60
193 aat tat aag acc atg tct act ctc tcc tgt gag aac aaa att att tcc 239
194 Asn Tyr Lys Thr Met Ser Thr Leu Ser Cys Glu Asn Lys Ile Ile Ser
195 65 70 75
197 ttt aag gaa atg agt cct cct gag agt atc aat gat gaa gga aat gac 287
198 Phe Lys Glu Met Ser Pro Pro Glu Ser Ile Asn Asp Glu Gly Asn Asp
199 80 85 90 95
201 atc ata ttc ttt cag aga agt gtt cca gga cat gat gat aag ata caa 335
202 Ile Ile Phe Phe Gln Arg Ser Val Pro Gly His Asp Asp Lys Ile Gln
203 100 105 110
205 ttt gag tct tca ttg tac aag ggg tac ttt cta gct tgt gaa aaa gag 383
206 Phe Glu Ser Ser Leu Tyr Lys Gly Tyr Phe Leu Ala Cys Glu Lys Glu
207 115 120 125
209 aaa gat ctt ttc aaa ctc att ttg aaa aaa aag gat gaa aat ggg gat 431
210 Lys Asp Leu Phe Lys Leu Ile Leu Lys Lys Lys Asp Glu Asn Gly Asp
211 130 135 140
213 aag tcc ata atg ttc act gtt caa aac aag aat tagatattaa aattgcataa 484

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```

214 Lys Ser Ile Met Phe Thr Val Gln Asn Lys Asn
215      145      150
217 tttgaaaaaa aaaaaaaa
220 <210> SEQ ID NO: 5
221 <211> LENGTH: 154
222 <212> TYPE: PRT
223 <213> ORGANISM: Felis catus
225 <220> FEATURE:
226 <221> NAME/KEY: misc_feature
227 <222> LOCATION: (42)..(42)
228 <223> OTHER INFORMATION: The 'Xaa' at location 42 stands for Thr, Ala, Pro, or Ser.
230 <400> SEQUENCE: 5
232 Lys Leu Glu His Lys Leu Ser Ile Leu Arg Asn Leu Asn Asp Gln Val
233 1      5      10      15
236 Leu Phe Ile Asn Gln Gly Asp Gln Pro Val Phe Glu Asp Met Pro Asp
237      20      25      30
W--> 240 Ser Asp Cys Thr Asp Asn Ala Pro Arg Xaa Glu Phe Ile Ile Tyr Met
241      35      40      45
244 Tyr Lys Asp Ser Leu Thr Arg Gly Leu Ala Val Thr Ile Ser Val Asn
245      50      55      60
248 Tyr Lys Thr Met Ser Thr Leu Ser Cys Glu Asn Lys Ile Ile Ser Phe
249 65      70      75      80
252 Lys Glu Met Ser Pro Pro Glu Ser Ile Asn Asp Glu Gly Asn Asp Ile
253      85      90      95
256 Ile Phe Phe Gln Arg Ser Val Pro Gly His Asp Asp Lys Ile Gln Phe
257      100     105     110
260 Glu Ser Ser Leu Tyr Lys Gly Tyr Phe Leu Ala Cys Glu Lys Glu Lys
261      115     120     125
264 Asp Leu Phe Lys Leu Ile Leu Lys Lys Lys Asp Glu Asn Gly Asp Lys
265      130     135     140
268 Ser Ile Met Phe Thr Val Gln Asn Lys Asn
269 145      150
272 <210> SEQ ID NO: 6
273 <211> LENGTH: 502
274 <212> TYPE: DNA
275 <213> ORGANISM: Felis catus
278 <220> FEATURE:
279 <221> NAME/KEY: misc_feature
280 <222> LOCATION: (377)..(377)
281 <223> OTHER INFORMATION: n = unknown at position 377
283 <400> SEQUENCE: 6
284 tttttttttt ttttcaaatt atgcaatttt aatatctaatt tcttggttttg aacagtgaac      60
286 attatggact tatccccatt ttcattccttt tttttcaaaa tgagtttgaa aagatctttc      120
288 tctttttcac aagctagaaa gtaccccttg tacaatgaag actcaaattg tatcttatca      180
290 tcatgtcctg gaacacttct ctgaaagaat atgatgtcat ttccttcatac attgatactc      240
292 tcaggaggac tcatttcctt aaaggaaata attttgttct cacaggagag agtagacatg      300
294 gtcttataat tcacagagat gggtactgcc agacctctag tgaggctatc tttatacata      360
W--> 296 tatatgataa attcagnccg ggggtgcatta tctgtacagt cagaatcagg catatcctca      420
298 aacacaggtt gatctccctg gttaatgaag agaacttggt cgttcaagtt tcgtaagatt      480

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```

300 gagagttttat gttcaagctt gc 502
303 <210> SEQ ID NO: 7
304 <211> LENGTH: 607
305 <212> TYPE: DNA
306 <213> ORGANISM: Felis catus
309 <220> FEATURE:
310 <221> NAME/KEY: CDS
311 <222> LOCATION: (24)..(599)
313 <400> SEQUENCE: 7
314 aactattgag cacagggata aag atg act gct ata cca gta gat gat tgc atc 53
315 Met Thr Ala Ile Pro Val Asp Asp Cys Ile
316 1 5 10
318 aac ttt gtg gga atg aaa ttt att gac aat aca ctt tac ttt gta gct 101
319 Asn Phe Val Gly Met Lys Phe Ile Asp Asn Thr Leu Tyr Phe Val Ala
320 15 20 25
322 gac agt gat gaa aac ctg gaa aca gat tac ttt ggc aag ctt gaa cat 149
323 Asp Ser Asp Glu Asn Leu Glu Thr Asp Tyr Phe Gly Lys Leu Glu His
324 30 35 40
326 aaa ctc tca atc tta cga aac ttg aac gac caa gtt ctc ttc att aac 197
327 Lys Leu Ser Ile Leu Arg Asn Leu Asn Asp Gln Val Leu Phe Ile Asn
328 45 50 55
330 cag gga gat caa cct gtg ttt gag gat atg cct gat tct gac tgt aca 245
331 Gln Gly Asp Gln Pro Val Phe Glu Asp Met Pro Asp Ser Asp Cys Thr
332 60 65 70
334 gat aat gca ccc cgg act gaa ttt atc ata tat atg tat aaa gat agc 293
335 Asp Asn Ala Pro Arg Thr Glu Phe Ile Ile Tyr Met Tyr Lys Asp Ser
336 75 80 85 90
338 ctc act aga ggt ctg gca gta acc atc tct gtg aat tat aag acc atg 341
339 Leu Thr Arg Gly Leu Ala Val Thr Ile Ser Val Asn Tyr Lys Thr Met
340 95 100 105
342 tct act ctc tcc tgt gag aac aaa att att tcc ttt aag gaa atg agt 389
343 Ser Thr Leu Ser Cys Glu Asn Lys Ile Ile Ser Phe Lys Glu Met Ser
344 110 115 120
346 cct cct gag agt atc aat gat gaa gga aat gac atc ata ttc ttt cag 437
347 Pro Pro Glu Ser Ile Asn Asp Glu Gly Asn Asp Ile Ile Phe Phe Gln
348 125 130 135
350 aga agt gtt cca gga cat gat gat aag ata caa ttt gag tct tca ttg 485
351 Arg Ser Val Pro Gly His Asp Asp Lys Ile Gln Phe Glu Ser Ser Leu
352 140 145 150
354 tac aag ggg tac ttt cta gct tgt gaa aaa gag aaa gat ctt ttc aaa 533
355 Tyr Lys Gly Tyr Phe Leu Ala Cys Glu Lys Glu Lys Asp Leu Phe Lys
356 155 160 165 170
358 ctc att ttg aaa aaa aag gat gaa aat ggg gat aag tcc ata atg ttc 581
359 Leu Ile Leu Lys Lys Lys Asp Glu Asn Gly Asp Lys Ser Ile Met Phe
360 175 180 185
362 act gtt caa aac aag aat tagatatt 607
363 Thr Val Gln Asn Lys Asn
364 190
367 <210> SEQ ID NO: 8

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RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/09/917,265A

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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:1; N Pos. 470
Seq#:1; Xaa Pos. 119
Seq#:2; Xaa Pos. 119
Seq#:3; N Pos. 45
Seq#:4; N Pos. 126
Seq#:4; Xaa Pos. 42
Seq#:5; Xaa Pos. 42
Seq#:6; N Pos. 377
Seq#:20; N Pos. 473
Seq#:22; N Pos. 28

Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete,
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:110